

Supplemental Table S3. Expression analysis of *CDA* isoforms based on RNA-seq data analysis.

	seedling (5 days) SRR1523305	rosette (21 days) SRR3136731 SRR3136732 SRR3136733	flower stage 1-9 SRR1104887 SRR1104888	flower stage 12 SRR1104889	inflorescence SRR1104149 SRR1104886	pollen SRR847501 SRR847502	silique SRR656219	root SRR656215
At2g19570.1	13.16	8.49	11.35	47.84	6.99	17.68	137.45	51.81
At4g29570.1	0	0.04	0.07	0.68	0.34	0	12.71	0
At4g29580.2	0.04	0	0.06	0.03	0.13	0	0.04	0
At4g29600.1	0.06	0	0	0.1	0	0	1.92	0
At4g29610.1	1.06	1.78	0.35	3.16	0.1	0	9.61	0.88
At4g29620.1	0	0.01	0	0	0	0	1.87	0
At4g29630.1	0	0	0	0	0	0.03	1.47	0
At4g29640.1	0	0	0	0.06	0	0	9.71	0.01
At4g29650.1	0	0.06	0	0.53	0.12	0	7.65	0.01

RNA-seq analysis of all *CDA* isoforms in different datasets obtained from the NCBI SRA (short read archive). RPKM (reads per million per kilobase of gene model) are shown for the respective tissues for each *CDA* gene indicating expression level. Only uniquely mapping reads from the data sets (accession numbers for each data set in the SRA are shown in the header) were considered for the analysis.